A2

Figure 1 provides an amino acid sequence alignment between ATPT2 (SEQ ID NO: 2), ATPT3 (SEQ ID NO: 4), ATPT4 (SEQ ID NO: 6), ATPT8 (SEQ ID NO: 12), and ATPT12 (SEQ ID NO: 17) performed using ClustalW.

Please delete the paragraph on page 4, beginning on line 25 and ending on line 26, and replace it with:

A3

Figure 21 provides an amino acid sequence alignment using ClustalW between the *Synechocystis* prenyltransferase sequences, slr1736 (SEQ ID NO: 37), slr0926 (SEQ ID NO: 32), sll1899 (SEQ ID NO: 33), slr0056 (SEQ ID NO: 34), and slr1518 (SEQ ID NO: 35).

Please delete the paragraph on page 4, beginning on line 27 and ending on line 29, and replace it with:

Figure 22 provides an amino acid sequence of the ATPT2 (SEQ ID NO: 2), ATPT3 (SEQ ID NO: 4), ATPT4 (SEQ ID NO: 6), ATPT8 (SEQ ID NO: 12), and ATPT12 (SEQ ID NO: 17) protein sequences from *Arabidopsis* and the slr1736 (SEQ ID NO: 37), slr0926 (SEQ ID NO: 32), sll1899 (SEQ ID NO: 33), slr0056 (SEQ ID NO: 34), and the slr1518 (SEQ ID NO: 35) amino acid sequences from *Synechocystis*.

Please delete the paragraph on page 5, beginning on line 19 and ending on line 20, and replace it with:

A4

Figure 31 is a sequence alignment of the *Arabidopsis* homologue (SEQ ID NO: 113) with the sequence of the public database (SEQ ID NO: 112).

Please delete the paragraph on page 5, beginning on line 25 and ending on line 26, and replace it with:

A5

Figure 35 is a sequence alignment of slr1737 (SEQ ID NO: 39), slr1737 *Arabidopsis* homologue (SEQ ID NO: 110) and the *Arabidopsis* chalcone isomerase (SEQ ID NO: 111).

Please delete the paragraphs spanning page 30, line 6 through line 15, and replace them with:

The sequence encoding ATPT2 prenyltransferase (SEQ ID NO: 1) was cloned in the sense orientation into pCGN8640 to produce the plant transformation construct pCGN10800 (Figure 2). The ATPT2 sequence is under control of the 35S promoter.

The ATPT2 sequence (SEQ ID NO: 1) was also cloned in the antisense orientation into the construct pCGN8641 to create pCGN10801 (Figure 3). This construct provides for the antisense expression of the ATPT2 sequence from the napin promoter.

The ATPT2 coding sequence (SEQ ID NO: 1) was also cloned in the sense orientation into the vector pCGN8643 to create the plant transformation construct pCGN10822.

The ATPT2 coding sequence (SEQ ID NO: 1) was also cloned in the antisense orientation into the vector pCGN8644 to create the plant transformation construct pCGN10803 (Figure 4).

Please delete the paragraph beginning on page 30, line 16, and ending on page 31, line 19, and replace it with:

The ATPT4 coding sequence (SEQ ID NO: 5) was cloned into the vector pCGN864 to create the plant transformation construct pCGN10806 (Figure 5). The ATPT2 coding sequence (SEQ ID NO: 1) was cloned into the vector TopoTA™ vector from Invitrogen, to create the plant transformation construct pCGN10807 (Figure 6). The ATPT3 (SEQ ID NO: 3) coding sequence was cloned into the TopoTA vector to create the plant transformation construct pCGN10808 (Figure 7). The ATPT3 (SEQ ID NO: 3) coding sequence was cloned in the sense orientation into the vector pCGN8640 to create the plant transformation construct pCGN10809 (Figure 8). The ATPT3 (SEQ ID NO: 3) coding sequence was cloned in the antisense orientation into the vector pCGN8641 to create the plant transformation construct pCGN10810 (Figure 9). The ATPT3 (SEQ ID NO: 3) coding sequence was cloned into the vector pCGN8643 to create the plant transformation construct pCGN10811 (Figure 10). The ATPT3 (SEQ ID NO: 3) coding sequence was cloned into the vector pCGN8644 to create the plant transformation construct pCGN10812 (Figure 11). The ATPT4 (SEQ ID NO: 5) coding sequence was cloned

into the vector pCGN8640 to create the plant transformation construct pCGN10813 (Figure 12). The ATPT4 (SEQ ID NO: 5) coding sequence was cloned into the vector pCGN8641 to create the plant transformation construct pCGN10814 (Figure 13). The ATPT4 (SEQ ID NO: 5) coding sequence was cloned into the vector pCGN8643 to create the plant transformation construct pCGN10815 (Figure 14). The ATPT4 (SEQ ID NO: 5) coding sequence was cloned in the antisense orientation into the vector pCGN8644 to create the plant transformation construct pCGN10816 (Figure 15). The ATPT8 (SEQ ID NO: 11) coding sequence was cloned in the sense orientation into the vector pCGN8643 to create the plant transformation construct pCGN10819 (Figure 17). The ATPT12 (SEQ ID NO: 16) coding sequence was cloned into the vector pCGN8640 to create the plant transformation construct pCGN10824 (Figure 18). The ATPT12 (SEQ ID NO: 16) coding sequence was cloned into the vector pCGN8643 to create the plant transformation construct pCGN10825 (Figure 19). The ATPT8 (SEQ ID NO: 11) coding sequence was cloned into the vector pCGN8640 to create the plant transformation construct pCGN10826 (Figure 20).

Please delete the paragraph on page 32, beginning on line 5 and ending on line 7, and replace it with:

Additional BLAST searches were performed using the ATPT2 sequence (SEQ ID NO: 1), a sequence in the class of aromatic prenyltransferases. ESTs, and in some cases, full-length coding regions, were identified in proprietary DNA libraries.

Please delete the paragraph on page 32, beginning on line 17 and ending on line 24, and replace it with:

A PSI-Blast profile generated using the *E. coli* ubiA (genbank accession 1790473) sequence was used to analyze the *Synechocystis* genome. This analysis identified 5 open reading frames (ORFs) in the *Synechocystis* genome that were potentially prenyltransferases; slr0926 (annotated as ubiA (4-hydroxybenzoate-octaprenyltransferase, SEQ ID NO:32)), sll1899 (annotated as ctaB (cytocrome c oxidase folding protein, SEQ ID NO:33)), slr0056 (annotated as g4 (chlorophyll synthase 33 kd subunit, SEQ ID NO:34)), slr1518 (annotated as menA

A8 Amended

(menaquinone biosynthesis protein, SEQ ID NO:35)), and slr1736 (annotated as a hypothetical protein of unknown function (SEQ ID NO: 37)).

Please delete the paragraph on page 36, beginning on line 20 and ending on line 22 and replace it with:

A9

The amino acid sequences for the *Synechocystis* knockouts, slr1736 (SEQ ID NO: 37), slr0926 (SEQ ID NO: 32), sll1899 (SEQ ID NO: 33), slr0056 (SEQ ID NO: 34), and slr1518 (SEQ ID NO: 35), are compared using ClustalW, and are provided in Table 3 below. Provided are the percent identities, percent similarity, and the percent gap. The alignment of the sequences is provided in Figure 21.

Please delete the paragraph on page 37, beginning on line 2 and ending on line 5, and replace it with:

A10

Amino acid sequence comparisons are performed using various *Arabidopsis* prenyltransferase sequences, ATPT2 (SEQ ID NO: 2), ATPT3 (SEQ ID NO: 4), ATPT4 (SEQ ID NO: 6), ATPT8 (SEQ ID NO: 12), and ATPT12 (SEQ ID NO: 17), and the *Synechocystis* sequences, slr1736 (SEQ ID NO: 37), slr0926 (SEQ ID NO: 32), sll1899 (SEQ ID NO: 33), slr0056 (SEQ ID NO: 34), and slr1518 (SEQ ID NO: 35). The comparisons are presented in Table 4 below. Provided are the percent identities, percent similarity, and the percent gap. The alignment of the sequences is provided in Figure 22.

Please delete the paragraph on page 48, beginning on line 11 and ending on line 15, and replace it with:

A11

The sequences obtained for the homologue from the proprietary database differs from the public database (F4D11.30, BAC AL022537), in having a start site 471 base pairs upstream of the start identified in the public sequence. A comparison of the public (SEQ ID NO: 112) and proprietary (SEQ ID NO: 113) sequences is provided in Figure 31. The correct start correlates within the public database sequence at 12080, while the public sequence start is given as being at 11609.

Please delete the paragraph beginning on page 48, line 24 and ending on page 49, line 3, and replace it with:

A12

The *Arabidopsis* homologue to slr1737 (SEQ ID NO: 110) comprises 488 amino acid residues, has a predicted MW of 55kDa, and has a putative transit peptide sequence comprising the first 98 amino acids. The predicted MW of the mature form of the *Arabidopsis* homologue is 44kDa. The hydropathic plot for the *Arabidopsis* homologue also reveals that it is hydrophillic (Figure 33). Further blast analysis of the *Arabidopsis* homologue reveals limited sequence identity (25% sequence identity) with the beta-subunit of respiratory nitrate reductase. Based on the sequence identity to nitrate reductase, it suggests the slr1737 ORF is an enzyme that likely involves general acid catalysis mechanism.

Please replace the paragraph on page 49, beginning on line 10 and ending on line 19, and replace it with:

A13

Multiple sequence alignment was performed between slr1737 (SEQ ID NO: 39), slr1737 *Arabidopsis* homologue (SEQ ID NO: 110) and the *Arabidopsis* chalcone isomerase (SEQ ID NO: 111) (Genbank:P41088) (Figure 35). Sixty-five percent of the conserved residues among the three enzymes are strictly conserved within the known chalcone isomerases. The crystal structure of alfalfa chalcone isomerase has been solved (Jez, Joseph M., Bowman, Marianne E., Dixon, Richard A., and Noel, Joseph P. (2000) "Structure and mechanism of the evolutionarily unique plant enzyme chalcone isomerase". *Nature Structural Biology* 7: 786-791.) It has been demonstrated that tyrosine (Y) 106 of the alfalfa chalcone isomerase serves as the general acid during cyclization reaction (Genbank: P28012). The equivalent residue in slr1737 (SEQ ID NO: 39), and the slr1737 *Arabidopsis* homologue (SEQ ID NO: 110) is lysine (K), which is an excellent catalytic residue as general acid.

In the Claims:

Please Amend the Claims as Follows: